



SEQLIST.txt

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANTS: June, Carl H., Thompson, Craig B., Nabel, Gary J.
Gray, Gary S., Rennert, Paul D.

(ii) TITLE OF INVENTION: Methods For Selectively Stimulating
Proliferation Of T-Cells

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: HALE AND DORR LLP
- (B) STREET: 60 State Street
- (C) CITY: Boston
- (D) STATE: Massachusetts
- (E) COUNTRY: USA
- (F) ZIP: 02109

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER: 09/349,915
- (B) FILING DATE: July 8, 1999
- (C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/403,253
- (B) FILING DATE: March 10, 1995
- (A) APPLICATION NUMBER: US 08/253,964
- (B) FILING DATE: 3 JUNE 1994
- (A) APPLICATION NUMBER: US 08/073,223
- (B) FILING DATE: 4 JUNE 1993
- (A) APPLICATION NUMBER: US 08/200,947
- (B) FILING DATE: 23 FEB 1994
- (A) APPLICATION NUMBER: US 07/864,805
- (B) FILING DATE: 7 APR 1992
- (A) APPLICATION NUMBER: US 08/247,505
- (B) FILING DATE: 23 MAY 1994
- (A) APPLICATION NUMBER: US 07/864,866
- (B) FILING DATE: 7 APR 1992
- (A) APPLICATION NUMBER: US 08/218,155
- (B) FILING DATE: 25 MAR 1994
- (A) APPLICATION NUMBER: US 07/864,807
- (B) FILING DATE: 7 APR 1992
- (A) APPLICATION NUMBER: US 07/902,467
- (B) FILING DATE: 16 JUNE 1992
- (A) APPLICATION NUMBER: US 07/275,433
- (B) FILING DATE: 23 NOV 1988

(viii) ATTORNEY/AGENT INFORMATION:

- (A) NAME: Superko, Colleen
- (B) REGISTRATION NUMBER: 39,850
- (C) REFERENCE/DOCKET NUMBER: 36119-125US8

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (617) 526-6564

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(B) TELEFAX: (617) 526-5000

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1491 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: no

(iv) ANTI-SENSE: no

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Homo sapien
- (F) TISSUE TYPE: lymphoid
- (G) CELL TYPE: B cell
- (H) CELL LINE: Raji

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: cDNA in pCDM8 vector
- (B) CLONE: B7, Raji clone #13

(viii) POSITION IN GENOME:

- (A) CHROMOSOME/SEGMENT: 3

(ix) FEATURE:

- (A) NAME/KEY: Open reading frame (translated region)
- (B) LOCATION: 318 to 1181 bp
- (C) IDENTIFICATION METHOD: similarity to other pattern

(ix) FEATURE:

- (A) NAME/KEY: Alternate polyadenylation signal
- (B) LOCATION: 1474 to 1479 bp
- (C) IDENTIFICATION METHOD: similarity to other pattern

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
WHITMAN, JAMES F.
NADLER, LEE M.
- (B) TITLE: B7, A New Member Of The Ig Superfamily With
Unique Expression On Activated And Neoplastic B Cells
- (C) JOURNAL: The Journal of Immunology
- (D) VOLUME: 143
- (E) ISSUE: 8
- (F) PAGES: 2714-2722
- (G) DATE: 15-OCT-1989
- (H) RELEVANT RESIDUES In SEQ ID NO:1: FROM 1 TO 1491

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

CCAAAGAAAA AGTGATTTGT CATTGCTTTA TAGACTGTAA GAAGAGAACA TCTCAGAAGT 60
GGAGTCTTAC CCTGAAATCA AAGGATTTAA AGAAAAAGTG GAATTTTCTCT TCAGCAAGCT 120
GTGAAACTAA ATCCACAACC TTTGGAGACC CAGGAACACC CTCCAATCTC TGTGTGTTTT 180
GTAAACATCA CTGGAGGGTC TTCTACGTGA GCAATTGGAT TGTCATCAGC CCTGCCTGTT 240
TTGCACCTGG GAAGTGCCCT GGTCTTACTT GGGTCCAAAT TGTTGGCTTT CACTTTTGAC 300
CCTAAGCATC TGAAGCC ATG GGC CAC ACA CGG AGG CAG GGA ACA TCA CCA TCC 353
Met Gly His Thr Arg Arg Gln Gly Thr Ser Pro Ser
-30 -25

AAG TGT CCA TAC CTG AAT TTC TTT CAG CTC TTG GTG CTG GCT GGT CTT 401
Lys Cys Pro Tyr Leu Asn Phe Phe Gln Leu Leu Val Leu Ala Gly Leu
-20 -15 -10

TCT CAC TTC TGT TCA GGT GTT ATC CAC GTG ACC AAG GAA GTG AAA GAA 449
Ser His Phe Cys Ser Gly Val Ile His Val Thr Lys Glu Val Lys Glu
-5 1 5 10

GTG GCA ACG CTG TCC TGT GGT CAC AAT GTT TCT GTT GAA GAG CTG GCA 497
Val Ala Thr Leu Ser Cys Gly His Asn Val Ser Val Glu Glu Leu Ala
15 20 25

CAA ACT CGC ATC TAC TGG CAA AAG GAG AAG AAA ATG GTG CTG ACT ATG 545
Gln Thr Arg Ile Tyr Trp Gln Lys Glu Lys Lys Met Val Leu Thr Met
30 35 40

ATG TCT GGG GAC ATG AAT ATA TGG CCC GAG TAC AAG AAC CGG ACC ATC 593
Met Ser Gly Asp Met Asn Ile Trp Pro Glu Tyr Lys Asn Arg Thr Ile
45 50 55

TTT GAT ATC ACT AAT AAC CTC TCC ATT GTG ATC CTG GCT CTG CGC CCA 641
Phe Asp Ile Thr Asn Asn Leu Ser Ile Val Ile Leu Ala Leu Arg Pro
60 65 70

TCT GAC GAG GGC ACA TAC GAG TGT GTT GTT CTG AAG TAT GAA AAA GAC 689
Ser Asp Glu Gly Thr Tyr Glu Cys Val Val Leu Lys Tyr Glu Lys Asp
75 80 85 90

GCT TTC AAG CGG GAA CAC CTG GCT GAA GTG ACG TTA TCA GTC AAA GCT 737
Ala Phe Lys Arg Glu His Leu Ala Glu Val Thr Leu Ser Val Lys Ala
95 100 105

GAC TTC CCT ACA CCT AGT ATA TCT GAC TTT GAA ATT CCA ACT TCT AAT 785
Asp Phe Pro Thr Pro Ser Ile Ser Asp Phe Glu Ile Pro Thr Ser Asn
110 115 120

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ATT	AGA	AGG	ATA	ATT	TGC	TCA	ACC	TCT	GGA	GGT	TTT	CCA	GAG	CCT	CAC	833
Ile	Arg	Arg	Ile	Ile	Cys	Ser	Thr	Ser	Gly	Gly	Phe	Pro	Glu	Pro	His	
		125					130					135				
CTC	TCC	TGG	TTG	GAA	AAT	GGA	GAA	GAA	TTA	AAT	GCC	ATC	AAC	ACA	ACA	881
Leu	Ser	Trp	Leu	Glu	Asn	Gly	Glu	Glu	Leu	Asn	Ala	Ile	Asn	Thr	Thr	
	140					145					150					
GTT	TCC	CAA	GAT	CCT	GAA	ACT	GAG	CTC	TAT	GCT	GTT	AGC	AGC	AAA	CTG	929
Val	Ser	Gln	Asp	Pro	Glu	Thr	Glu	Leu	Tyr	Ala	Val	Ser	Ser	Lys	Leu	
155					160					165					170	
GAT	TTC	AAT	ATG	ACA	ACC	AAC	CAC	AGC	TTC	ATG	TGT	CTC	ATC	AAG	TAT	977
Asp	Phe	Asn	Met	Thr	Thr	Asn	His	Ser	Phe	Met	Cys	Leu	Ile	Lys	Tyr	
				175					180					185		
GGA	CAT	TTA	AGA	GTG	AAT	CAG	ACC	TTC	AAC	TGG	AAT	ACA	ACC	AAG	CAA	1025
Gly	His	Leu	Arg	Val	Asn	Gln	Thr	Phe	Asn	Trp	Asn	Thr	Thr	Lys	Gln	
			190					195					200			
GAG	CAT	TTT	CCT	GAT	AAC	CTG	CTC	CCA	TCC	TGG	GCC	ATT	ACC	TTA	ATC	1073
Glu	His	Phe	Pro	Asp	Asn	Leu	Leu	Pro	Ser	Trp	Ala	Ile	Thr	Leu	Ile	
		205				210						215				
TCA	GTA	AAT	GGA	ATT	TTT	GTG	ATA	TGC	TGC	CTG	ACC	TAC	TGC	TTT	GCC	1121
Ser	Val	Asn	Gly	Ile	Phe	Val	Ile	Cys	Cys	Leu	Thr	Tyr	Cys	Phe	Ala	
	220					225					230					
CCA	AGA	TGC	AGA	GAG	AGA	AGG	AGG	AAT	GAG	AGA	TTG	AGA	AGG	GAA	AGT	1169
Pro	Arg	Cys	Arg	Glu	Arg	Arg	Arg	Asn	Glu	Arg	Leu	Arg	Arg	Glu	Ser	
235				240					245					250		
GTA	CGC	CCT	GTA	TAACAGT	GTG	CGCAGAAGCA	AGGGGCTGAA	AAGATCTGAA								1221
Val	Arg	Pro	Val													
GGTAGCCTCC	GTCATCTCTT	CTGGGATACA	TGGATCGTGG	GGATCATGAG	GCATTCTTCC											1281
CTTAACAAAT	TTAAGCTGTT	TTACCCACTA	CCTCACCTTC	TTAAAAACCT	CTTTCAGATT											1341
AAGCTGAACA	GTTACAAGAT	GGCTGGCATC	CCTCTCCTTT	CTCCCCATAT	GCAATTTGCT											1401
TAATGTAACC	TCTTCTTTTG	CCATGTTTCC	ATTCTGCCAT	CTTGAATTGT	CTTGTCAGCC											1461
AATTCATTAT	CTATTAAACA	CTAATTTGAG														1491

(3) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 288 amino acids

g

- (B) TYPE: amino acid
- (C) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

- (A) DESCRIPTION: B cell activation antigen; natural ligand for CD28 T cell surface antigen; transmembrane protein

(ix) FEATURE:

- (A) NAME/KEY: signal sequence
- (B) LOCATION: -34 to -1
- (C) IDENTIFICATION METHOD: amino terminal sequencing of soluble protein
- (D) OTHER INFORMATION: hydrophobic

(ix) FEATURE:

- (A) NAME/KEY: extracellular domain
- (B) LOCATION: 1 to 208
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: transmembrane domain
- (B) LOCATION: 209 to 235
- (C) IDENTIFICATION METHOD: similarity with known sequence

g7 (ix) FEATURE:

- (A) NAME/KEY: intracellular domain
- (B) LOCATION: 236 to 254
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 19 to 21
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 55 to 57
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 64 to 66
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 152 to 154
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 173 to 175
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 177 to 179
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- gn
- (A) NAME/KEY: N-linked glycosylation
 - (B) LOCATION: 192 to 194
 - (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: N-linked glycosylation
- (B) LOCATION: 198 to 200
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: Ig V-set domain
- (B) LOCATION: 1 to 104
- (C) IDENTIFICATION METHOD: similarity with known sequence

(ix) FEATURE:

- (A) NAME/KEY: Ig C-set domain
- (B) LOCATION: 105 to 202
- (C) IDENTIFICATION METHOD: similarity with known sequence

(x) PUBLICATION INFORMATION:

- (A) AUTHORS: FREEMAN, GORDON J.
FREEDMAN, ARNOLD S.
SEGIL, JEFFREY M.
LEE, GRACE
WHITMAN, JAMES F.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Ile	Phe	Val	Ile	Cys	Cys	Leu	Thr	Tyr	Cys	Phe	Ala	Pro	Arg	Cys	Arg
		225					230					235			
Glu	Arg	Arg	Arg	Asn	Glu	Arg	Leu	Arg	Arg	Glu	Ser	Val	Arg	Pro	Val
	240					245					250				

(2) INFORMATION FOR SEQ ID NO:3:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 1120 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

- (ix) FEATURE:
- (A) NAME/KEY: CDS
 - (B) LOCATION: 107..1093

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CACAGGGTGA AAGCTTTGCT TCTCTGCTGC TGTAACAGGG ACTAGCACAG ACACACGGAT	60
GAGTGGGGTC ATTTCCAGAT ATTAGGTCAC AGCAGAAGCA GCCAAA ATG GAT CCC	115
	Met Asp Pro
	1
CAG TGC ACT ATG GGA CTG AGT AAC ATT CTC TTT GTG ATG GCC TTC CTG	163
Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met Ala Phe Leu	
	5 10 15
CTC TCT GGT GCT GCT CCT CTG AAG ATT CAA GCT TAT TTC AAT GAG ACT	211
Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe Asn Glu Thr	
	20 25 30 35
GCA GAC CTG CCA TGC CAA TTT GCA AAC TCT CAA AAC CAA AGC CTG AGT	259
Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln Ser Leu Ser	
	40 45 50
GAG CTA GTA GTA TTT TGG CAG GAC CAG GAA AAC TTG GTT CTG AAT GAG	307
Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val Leu Asn Glu	
	55 60 65
GTA TAC TTA GGC AAA GAG AAA TTT GAC AGT GTT CAT TCC AAG TAT ATG	355
Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser Lys Tyr Met	
	70 75 80
GGC CGC ACA AGT TTT GAT TCG GAC AGT TGG ACC CTG AGA CTT CAC AAT	403
Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg Leu His Asn	
	85 90 95
CTT CAG ATC AAG GAC AAG GGC TTG TAT CAA TGT ATC ATC CAT CAC AAA	451
Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile His His Lys	
	100 105 110 115
AAG CCC ACA GGA ATG ATT CGC ATC CAC CAG ATG AAT TCT GAA CTG TCA	499
Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser Glu Leu Ser	
	120 125 130

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GTG CTT GCT AAC TTC AGT CAA CCT GAA ATA GTA CCA ATT TCT AAT ATA	547
Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile Ser Asn Ile	
	135
	140
	145
ACA GAA AAT GTG TAC ATA AAT TTG ACC TGC TCA TCT ATA CAC GGT TAC	595
Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile His Gly Tyr	
	150
	155
	160
CCA GAA CCT AAG AAG ATG AGT GTT TTG CTA AGA ACC AAG AAT TCA ACT	643
Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys Asn Ser Thr	
	165
	170
	175
ATC GAG TAT GAT GGT ATT ATG CAG AAA TCT CAA GAT AAT GTC ACA GAA	691
Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn Val Thr Glu	
	180
	185
	190
	195
CTG TAC GAC GTT TCC ATC AGC TTG TCT GTT TCA TTC CCT GAT GTT ACG	739
Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro Asp Val Thr	
	200
	205
	210
AGC AAT ATG ACC ATC TTC TGT ATT CTG GAA ACT GAC AAG ACG CGG CTT	787
Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys Thr Arg Leu	
	215
	220
	225
TTA TCT TCA CCT TTC TCT ATA GAG CTT GAG GAC CCT CAG CCT CCC CCA	835
Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln Pro Pro Pro	
	230
	235
	240
GAC CAC ATT CCT TGG ATT ACA GCT GTA CTT CCA ACA GTT ATT ATA TGT	883
Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val Ile Ile Cys	
	245
	250
	255
GTG ATG GTT TTC TGT CTA ATT CTA TGG AAA TGG AAG AAG AAG AAG CGG	931
Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys Lys Lys Arg	
	260
	265
	270
	275
CCT CGC AAC TCT TAT AAA TGT GGA ACC AAC ACA ATG GAG AGG GAA GAG	979
Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu Arg Arg Glu	
	280
	285
	290
AGT GAA CAG ACC AAG AAA AGA GAA AAA ATC CAT ATA CCT GAA AGA TCT	1027
Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro Glu Arg Ser	
	295
	300
	305
GAT GAA GCC CAG CGT GTT TTT AAA AGT TCG AAG ACA TCT TCA TGC GAC	1075
Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser Ser Cys Asp	
	310
	315
	320
AAA AGT GAT ACA TGT TTT TAATTAAAGA GTAAAGCCCA AAAAAAA	1120
Lys Ser Asp Thr Cys Phe	
	325

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

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Met Asp Pro Gln Cys Thr Met Gly Leu Ser Asn Ile Leu Phe Val Met
1 5 10 15
Ala Phe Leu Leu Ser Gly Ala Ala Pro Leu Lys Ile Gln Ala Tyr Phe
20 25 30
Asn Glu Thr Ala Asp Leu Pro Cys Gln Phe Ala Asn Ser Gln Asn Gln
35 40 45
Ser Leu Ser Glu Leu Val Val Phe Trp Gln Asp Gln Glu Asn Leu Val
50 55 60
Leu Asn Glu Val Tyr Leu Gly Lys Glu Lys Phe Asp Ser Val His Ser
65 70 75 80
Lys Tyr Met Gly Arg Thr Ser Phe Asp Ser Asp Ser Trp Thr Leu Arg
85 90 95
Leu His Asn Leu Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Ile Ile
100 105 110
His His Lys Lys Pro Thr Gly Met Ile Arg Ile His Gln Met Asn Ser
115 120 125
Glu Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Val Pro Ile
130 135 140
Ser Asn Ile Thr Glu Asn Val Tyr Ile Asn Leu Thr Cys Ser Ser Ile
145 150 155 160
His Gly Tyr Pro Glu Pro Lys Lys Met Ser Val Leu Leu Arg Thr Lys
165 170 175
Asn Ser Thr Ile Glu Tyr Asp Gly Ile Met Gln Lys Ser Gln Asp Asn
180 185 190
Val Thr Glu Leu Tyr Asp Val Ser Ile Ser Leu Ser Val Ser Phe Pro
195 200 205
Asp Val Thr Ser Asn Met Thr Ile Phe Cys Ile Leu Glu Thr Asp Lys
210 215 220
Thr Arg Leu Leu Ser Ser Pro Phe Ser Ile Glu Leu Glu Asp Pro Gln
225 230 235 240
Pro Pro Pro Asp His Ile Pro Trp Ile Thr Ala Val Leu Pro Thr Val
245 250 255
Ile Ile Cys Val Met Val Phe Cys Leu Ile Leu Trp Lys Trp Lys Lys
260 265 270
Lys Lys Arg Pro Arg Asn Ser Tyr Lys Cys Gly Thr Asn Thr Met Glu
275 280 285
Arg Glu Glu Ser Glu Gln Thr Lys Lys Arg Glu Lys Ile His Ile Pro
290 295 300
Glu Arg Ser Asp Glu Ala Gln Arg Val Phe Lys Ser Ser Lys Thr Ser
305 310 315 320
Ser Cys Asp Lys Ser Asp Thr Cys Phe

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 1
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 3
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 7
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 8
- (D) OTHER INFORMATION: /label=Xaa is Asp or Glu

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 9
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Xaa Gly Xaa Trp Leu Xaa Xaa Xaa Xaa
5

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 227 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Pro Val Lys Gly Gly Thr Lys Cys Ile Lys Tyr Leu Leu Phe Gly Phe
5 10 15

Asn Phe Ile Phe Trp Leu Ala Gly Ile Ala Val Leu Ala Ile Gly Leu
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20 25 30

Trp Leu Arg Phe Asp Ser Gln Thr Lys Ser Ile Phe Glu Gln Glu Thr
35 40 45

Asn Asn Asn Asn Ser Ser Phe Tyr Thr Gly Val Tyr Ile Leu Ile Gly
50 55 60

Ala Gly Ala Leu Met Met Leu Val Gly Phe Leu Gly Cys Cys Gly Ala
65 70 75 80

Val Gln Glu Ser Gln Cys Met Leu Gly Leu Phe Phe Gly Phe Leu Leu
85 90 95

Val Ile Phe Ala Ile Glu Ile Ala Ala Ala Ile Trp Gly Tyr Ser His
100 105 110

Lys Asp Glu Val Ile Lys Glu Val Gln Glu Phe Tyr Lys Asp Thr Tyr
115 120 125

Asn Lys Leu Lys Thr Lys Asp Glu Pro Gln Arg Glu Thr Leu Lys Ala
130 135 140

Ile His Tyr Ala Leu Asn Cys Cys Gly Leu Ala Gly Gly Val Glu Gln
145 150 155 160

Phe Ile Ser Asp Ile Cys Pro Lys Lys Asp Val Leu Glu Thr Phe Thr
165 170 175

Val Lys Ser Cys Pro Asp Ala Ile Lys Glu Val Phe Asp Asn Lys Phe
180 185 190

His Ile Ile Gly Ala Val Gly Ile Gly Ile Ala Val Val Met Ile Phe
195 200 205

Gly Met Ile Phe Ser Met Ile Leu Cys Cys Ala Ile Arg Arg Asn Arg
210 215 220

Glu Met Val
225

(2) INFORMATION FOR SEQ ID NO:7:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Gly Leu Trp Leu Arg Phe Asp
1 5

(2) INFORMATION FOR SEQ ID NO:8:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20 amino acids

97

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

His Gln Phe Cys Asp His Trp Gly Cys Trp Leu Leu Arg Glu Thr His
1 5 10 15
Ile Phe Thr Pro
20

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Leu Arg Leu Val Leu Glu Asp Pro Gly Ile Trp Leu Arg Pro Asp Tyr
1 5 10 15
Phe Phe Pro Ala
20

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Gly Cys Trp Leu Leu Arg Glu
1 5

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 7 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly Ile Trp Leu Arg Pro Asp
1 5

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 6 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 2
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 5
- (D) OTHER INFORMATION: /label=Xaa is any amino acid

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION: 6
- (D) OTHER INFORMATION: /label=Xaa is Asp or Glu

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Gly Xaa Trp Leu Xaa Xaa
1 5

(2) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

CTTTAGAGCA CA

12

(2) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

SEQLIST.txt

97 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

CTCTAAAG

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